

## Phylogenetic Distance Tree<sup>IMG 3.2</sup>

Genomes are first selected for distance tree calculation (Figure 1). The program then computes the distances and displays the tree in the [Archaeopterix applet](#) (Figure 2). This applet allows users to save the analyzed tree as a PDF file. Each node in the tree links to the gene page for that node.

IMG HomeFind GenomesFind GenesFind FunctionsCompare GenomesAnalysis CartsMyIMG

Genome Statistics | Synteny Viewers | Distance Tree | Abundance Profiles | Function Profile | Genome Clustering

### Distance Tree

Loaded.

Please select genomes for the tree.

Reset

Select	Ignore	Taxon Name
<input checked="" type="radio"/>	<input type="radio"/>	<b>Archaea</b>
<input checked="" type="radio"/>	<input type="radio"/>	<b>Crenarchaeota</b>
<input checked="" type="radio"/>	<input type="radio"/>	<b>Aeropyrum</b>
<input checked="" type="radio"/>	<input type="radio"/>	<a href="#">Aeropyrum pernix K1</a> (A)[F]
<input checked="" type="radio"/>	<input type="radio"/>	<b>Desulfurococcus</b>
<input checked="" type="radio"/>	<input type="radio"/>	<a href="#">Desulfurococcus kamchatkensis 1221n</a> (A)[F]
<input type="radio"/>	<input type="radio"/>	<b>Nematoda</b>
<input type="radio"/>	<input type="radio"/>	<b>Caenorhabditis</b>
<input type="radio"/>	<input checked="" type="radio"/>	<a href="#">Caenorhabditis elegans</a> (E)[F]
<input type="radio"/>	<input type="radio"/>	<b>Streptophyta</b>
<input type="radio"/>	<input type="radio"/>	<b>Arabidopsis</b>
<input type="radio"/>	<input checked="" type="radio"/>	<a href="#">Arabidopsis thaliana</a> (E)[F]

Distance Tree

**Figure 1.** Distance Tree – Genome Selection

## Phylogenetic Tree for Selected Genomes

The tree below is generated using the [Archaeopteryx](#) applet

[Launch in separate window](#)

[View phyloXML](#)



**Figure 2.** Distance tree viewed in the embedded Archaeopteryx applet

The user can also choose to download the [phyloXML](#) file of the tree.

## Phylogenetic Distance Tree - Integration IMG 3.3

### Gene Homologs

“Phylogenetic Distribution” button on the Gene Homologs page now links to the [Archaeopterix applet](#) (Figure 3a), used to display the phylogenetic tree. This tree is colored by the count of homologs (Figure 3b).

#### Gene Homolog

[Customized Homolog Display](#)

**Homolog Selection** Top IMG Homolog Hits

#### Top IMG Homolog Hits

Phylogenetic Distribution

Types (T): O = Ortholog, P = Paralog, H - Putative origin of Horizontal Transfer, - = other unidirectional hit.  
Domains(D): B=Bacteria, A=Archaea, E=Eukarya, P=Plasmids, V=Viruses.  
Genome Completion(C): F=Finished, P=Permanent Draft, D=Draft.

☒ Add query gene [638158342](#)

Add Selections To Gene Cart

Select All

Clear All

Search column: Bit Score Search term:

Export

Page 1 of 3 << first < prev 1 2 3 next > last >> 100

Column Selector

Select Page

Deselect Page

Select	Homolog	T	Percent Identity	Length	E-value	Bit Score	Domain	Status	Genome Name
<input type="checkbox"/>	<a href="#">648021755</a>	O	58.43	524aa	5.0e-166	587.0	A	F	<a href="#">Ferroglobus placidus DSM 10642</a>
<input type="checkbox"/>	<a href="#">638187665</a>	O	53.42	538aa	1.0e-147	517.0	A	F	<a href="#">Aeropyrum pernix K1</a>
<input type="checkbox"/>	<a href="#">640820074</a>	O	46.26	523aa	8.0e-119	430.0	B	F	<a href="#">Nitratiruptor sp. SB155-2</a>
<input type="checkbox"/>	<a href="#">647586885</a>	O	51.19	434aa	1.0e-116	423.0	A	D	<a href="#">Aciduliprofundum boonei T469</a>
<input type="checkbox"/>	<a href="#">647586746</a>	-	50.95	434aa	3.0e-116	421.0	A	D	<a href="#">Aciduliprofundum boonei T469</a>

**Figure 3a.** Gene Homologs link to [Archaeopterix applet](#).

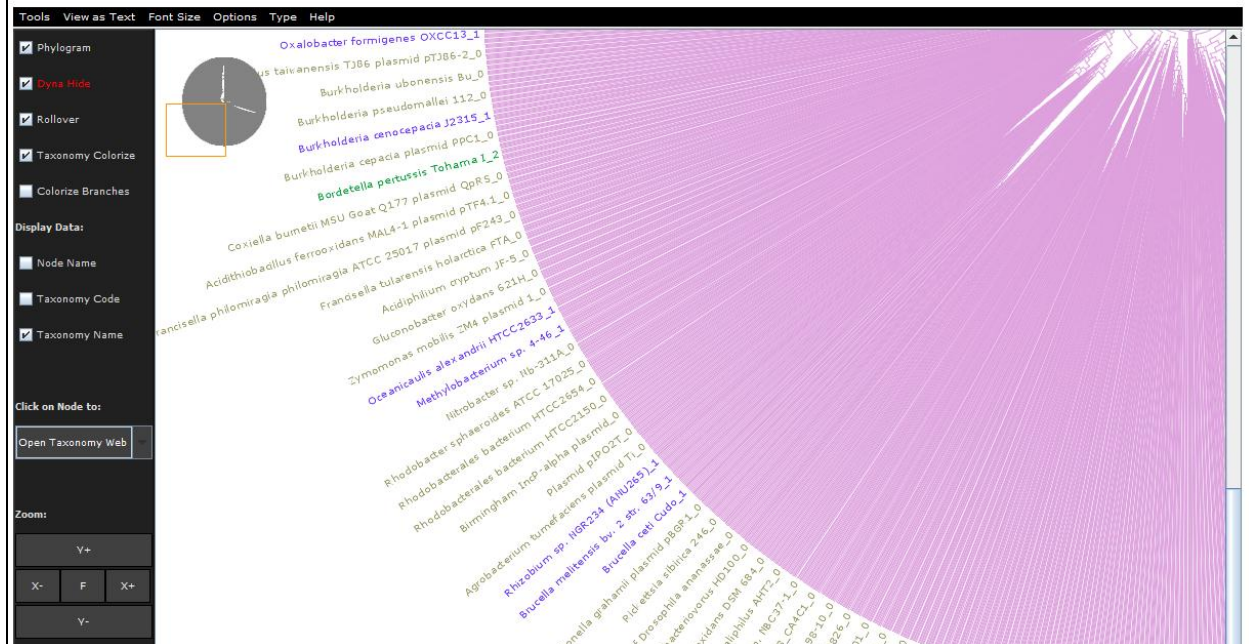
## Phylogenetic Tree for All Genomes

Displaying homologs for gene: [637112107](#)

[ homolog counts: 0, 1, 2, >2 ]

3631 genomes were analyzed  
The tree below is generated using the [Archaeopteryx](#) applet

Launch in separate window

[View phyloXML](#)

**Figure 3b.** Gene Homolog counts displayed in [Archaeopterix applet](#).

# Hierarchical Genome Clustering

Genome Clustering now also links to the [Archaeopterix applet](#) (Figure 4).

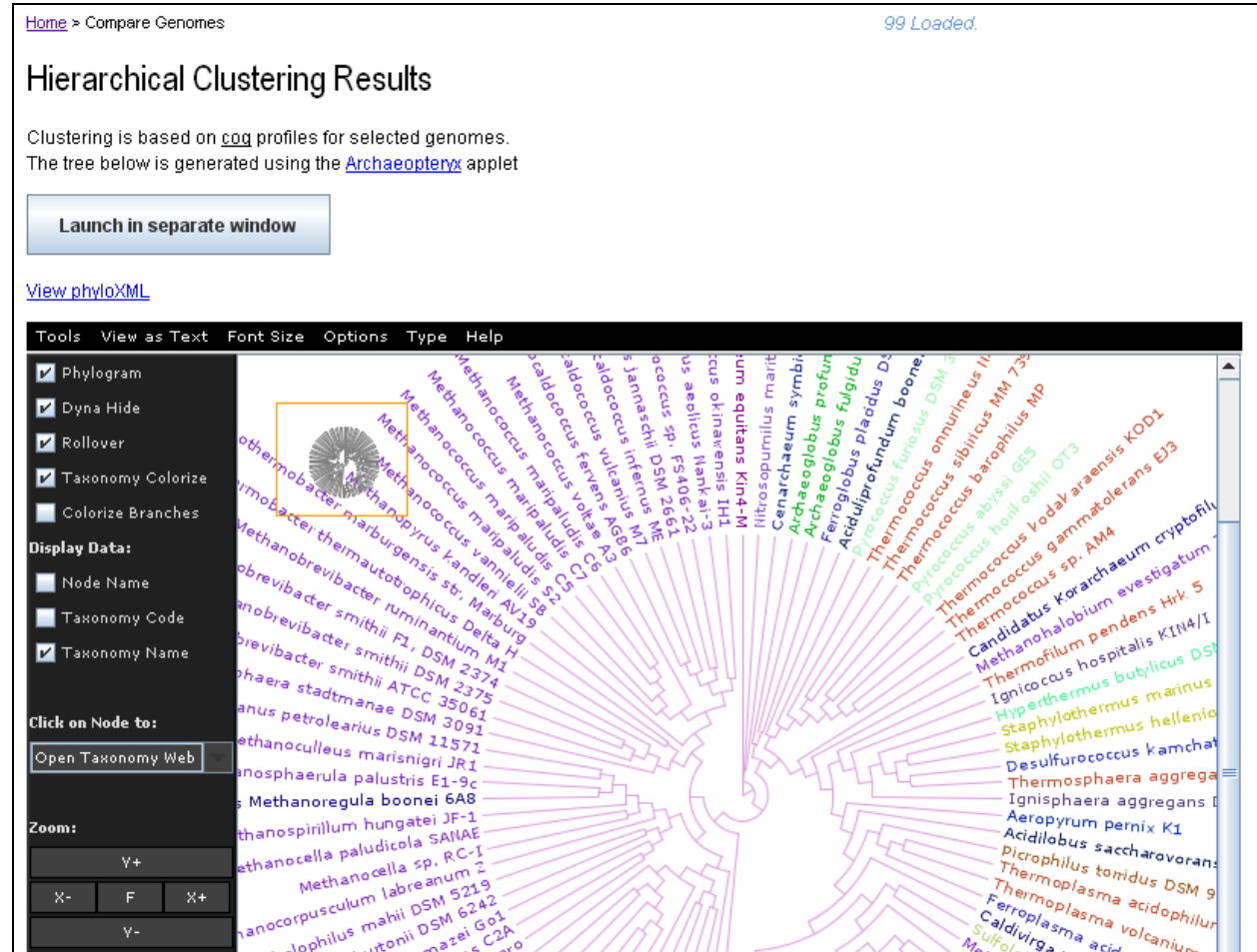
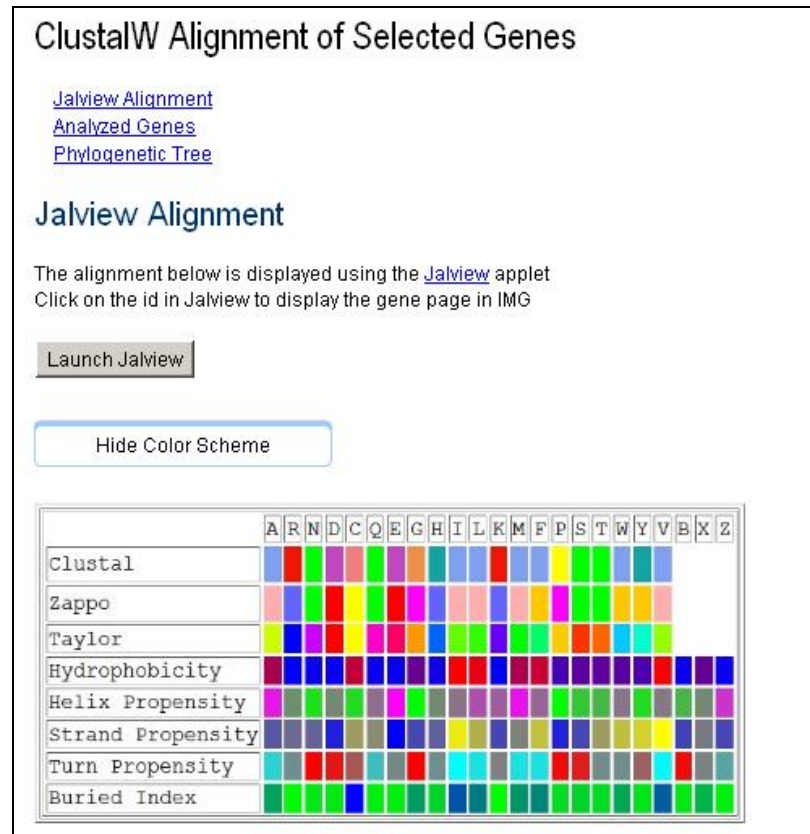


Figure 4. Genome Clustering using the [Archaeopterix applet](#).

## ClustalW Alignment

From the Gene Cart, the user can choose to do Sequence Alignment on selected genes. This alignment is displayed using the Jalview applet, which is now embedded (Figure 5b). Clicking on the gene in Jalview, opens up a Gene Details page in IMG.



**Figure 5a.** Jalview Color Scheme for amino acid sequence alignment



